

transducer and activator of transcription (STAT)1, STAT2 and STAT3
 Biochem. J. 370 (Pt 2), 391-396 (2003)
 JOURNAL
 MEDLINE 22478845
 PUBMED 12521379
 REFERENCE 2 (bases 1 to 1476)
 AUTHORS Renaud, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (06-DEC-2002) Renaud J.C., UCL 74.59, Ludwig Institute
 for Cancer Research, 74 Avenue Hippocrate, B-1200 Brussels, BELGIUM
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 (LIGR2 gene).
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 VERSION AJ534330.1 GI:26986037
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Mon Sep 22 11:34:33 2003

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Page 4

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ACCESSION	AF439325		
VERSION	AF439325.1	GI:24637276	
KEYWORDS			
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	1 (bases 1 to 4536)		
AUTHORS	Gallagher, G. and Kotenko, S.		
JOURNAL	CRF2/12 is a novel member of the class-II cytokine receptor family		
REFERENCE	unpublished		
AUTHORS	2 (bases 1 to 4536)		
AUTHORS	Gallagher, G. and Kotenko, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-OCT-2001) Dental Research Centre, NIDS / Dept. of Biochemistry and Molecular Biology, NMS, University of Medicine and Dentistry of New Jersey, 185 South Orange Avenue, Newark, NJ 07103-2774, USA		
REMARK	This is joint work from G. Gallagher and S. Kotenko		
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REFERENCE	1 Presnell, S.R., Xu, W., Novak, J.E., Whitmore, T.B. and Grant, P.J.		
AUTHORS	Cytokine receptor zyc7c019		
TITLE	Patent: WO 0244209-A 18 06-JUN-2002;		
JOURNAL	ZymoGenetics, Inc. (US)		
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Preenell, S.R., Xu, W., Novak, J.E., Whitmore, T.E. and Grant, F.J.
 Cytokine receptor zcytor1
 Patent: WO 0244209-A 1 06-JUN-2002;

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 BASE COUNT 309 a 439 c 456 g 272 t
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 Query Match 85.5%, Score 1259, DB 6, Length 1476;
 Best Local Similarity 92.8%, Pred. No. 5.2e-111;
 Matches 1372; Conservative 0; Mismatches 60; Indels 47; Gaps 3;

QY 7 ATGCGGGGCGGAGCGTGGAGGCGCCCTGCTCTGTGCTCTGCTCAGCGCTCAAGG 66
 Db 1 ATGCGGGGCGGAGCGTGGAGGCGCCCTGCTCTGTGCTCTGCTCAGCGCTCAAGG 60
 QY 67 AGGCCCGCTGGCCCTCCCAAGATGAGCTGCTCCAGAACTTCAAGGCTGAC 126
 Db 61 AGGCCCGCTGGCCCTCCCAAGATGAGCTGCTCCAGAACTTCAAGGCTGAC 120
 QY 127 CTGACATGCTCCAGAGCTTGGCAACCCCAAGATGTAACCTATTGTCCTATCAG 186
 Db 121 CTGACATGCTCCAGAGCTTGGCAACCCCAAGATGTAACCTATTGTCCTATCAG 180
 QY 187 AGCTTCCCAACCGGTGACCGGTGGCGGAGTGAAGAGTGGCGGAAACCAAGAGCTG 246
 Db 181 AGCTTCCCAACCGGTGACCGGTGGCGGAGTGAAGAGTGGCGGAAACCAAGAGCTG 240
 QY 247 CTATGTTCTATGATGTGCTGAGAAACAGAGCTGTACAAGTTCAAGGAGCGGTG 306
 Db 241 CTATGTTCTATGATGTGCTGAGAAACAGAGCTGTACAAGTTCAAGGAGCGGTG 300
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 QY 367 TTTGAATGAGAGCGGCGCCCACTGTCTGTGCTCAACCAAGAGAGATCTGAGT 426
 Db 361 TTTGAATGAGAGCGGCGCCCACTGTCTGTGCTCAACCAAGAGAGATCTGAGT 420
 QY 427 GCAATGCACTGACAGCTGCGCCCTGATGCGCCCACTGAGATCTGAAGATGAGGTG 486
 Db 421 GCAATGCACTGACAGCTGCGCCCTGATGCGCCCACTGAGATCTGAAGATGAGGTG 480
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 QY 667 GAGTCCAGAGACTTTCTGAGACAC-----A 694

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Db 721 GTAATTCGCGAGGGGTGTGATCTGGAAGACCTTCAATGGGAAACCCCTGTTCAGCGG 780
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Db 781 GCMAAGATGCAAGGCGCTTGGATCTGACAGAGGGTCAAGCCGACGCTTCAAGTCAAG 840
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Qy 863 GATGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 922
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RESULT 8
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LOCUS AX478499
DEFINITION Sequence 3 from Patent WO0244209.
ACCESSION AX478499
VERSION AX478499.1 GI:22217275
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Presnell, S.R., Xu, W., Novak, J.B., Whitmore, T.B. and Grant, F.J.
AUTHORS
TITLE Cytokine receptor zcytor19
JOURNAL Patent: WO 0244209-A 3 06-JUN-2002;
ZymoGenetics, Inc. (US)
FEATURES
Location/Qualifiers
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source
1..1473
/organism="synthetic construct"

Query Match 58.5%; Score 861.8; DB 6; Length 1473;
Best Local Similarity 52.5%; Pred. No. 2.2e-209;
Matches 775; Conservative 320; Mismatches 333; Indels 47; Gaps 3;
BASE COUNT 203 a 195 c 278 g 164 t 633 others
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/note="Degenerate polynucleotide sequence of SEQ ID NO:2"

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Qy 127 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
Db 121 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
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Db 901 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

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 QY 983 AGGCCAGGCTCTCTGCTGCTCCAGGAAAGGCTCTCTGCTGGAATTTCAAGACGA 1042
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 QY 1043 AGCTGGGCGACGACGCTGGAAGCTCTCTGCTGGAAGGCTGCTCTGCTGCTGCTGCT 1102
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RESULT 9
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 LOCUS AX478524 Sequence 28 from Patent WO0244209.
 DEFINITION AX478524
 ACCESSION AX478524.1 GI:22217296
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 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
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BASE COUNT 221 a 209 c 286 g 173 t 671 others
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Query Match 57.9%; Score 852.6; DB 6; Length 1560;
 Best Local Similarity 51.9%; Pred. No. 4.9e-207;
 Matches 810; Conservative 331; Mismatches 287; Indels 134; Gaps 2;

QY 7 ATGAGGAGGCGGAGCGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66
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 QY 187 AGCTCTCCACCTGAGACGCTGGGCGGAGATGGAAGATGCTGGGGAACCAAGAGCTG 246
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 DB 301 MGNACGNTGMSNCCNMSNMSNAARMSNCCNTGGGTGAGMSNARTATYTTGATTAAT 360
 QY 367 TTTGAGATGAGCGCGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
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 RESULT 10
 AL590683/C 164684 bp DNA linear PRI 01-FEB-2002
 LOCUS Human DNA sequence from clone RP11-10N16 on chromosome 1, complete
 DEFINITION
 ACCESSION AL590683
 VERSION AL590683.16 GI:18476679
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 164684)
 Chapman J.
 Direct Submission
 Submitted (01-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 hummery@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
 On Feb 1, 2002 this sequence version replaced 91:18135066.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Bm, EMBL, SW;
 SWISSPROT; Tr, TrEMBL; Mp, MOPREP; Information on the MOPREP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr1
 RP11-10N16 is from the library RP11-11 constructed by the group
 of Pieter de Jong. For further details see

http://www.choil.org/bacpac/home.htm
 VECTOR: pAC3.6
 This sequence is the entire insert of clone RP11-10N16. The true
 left end of clone RP11-509P14 is at 17440 in this sequence. The
 true right end of clone RP11-293P20 is at 7865 in this sequence.
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 Best Local Similarity 99.6%; Pred. No. 2.9e-189;
 Matches 796; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
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 QY 1454 CATCCACCGAATCTGATG 1472
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RESULT 11

AX478518

LOCUS AX478518 1422 bp DNA linear PAT 12-AUG-2002
 DEFINITION Sequence 22 from Patent WO0244209.
 ACCESSION AX478518
 VERSION AX478518.1 GI:22217290

KEYWORDS

SYNTHETIC CONSTRUCT

SYNTHETIC CONSTRUCT

ARTIFICIAL SEQUENCES

ORGANISM

1

PRESNELL, S.R., XU, W., NOVAK, J.E., WHITMORE, T.E. and GRANT, F.J.

CYTOKINE RECEPTOR ZCYTOR19

PATENT: WO 0244209-A 22 06-JUN-2002;

ZymoGenetics, Inc. (US)

LOCATION/Qualifiers

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BASE COUNT 331 a 451 c 377 g 263 t

ORIGIN

Query Match 41.6%; Score 612.8; DB 6; Length 1422;

Best Local Similarity 98.9%; Pred. No. 1.1e-145;

Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 67 AGCCCCCTCTGGGCCCCCTCCCGAATGTGACGCTGCTCTCCCGAATCTCAAGCTGTAC 126

DB 109 AGCCCCCTCTGGGCCCCCTCCCGAATGTGACGCTGCTCTCCCGAATCTCAAGCTGTAC 168

QY 127 CTGACATGGCTCCGAGGCTTGGCAACCCCGAGATGTGACCTATTTTGGGCTATCAG 186

DB 169 CTGACATGGCTCCGAGGCTTGGCAACCCCGAGATGTGACCTATTTTGGGCTATCAG 228

QY 187 AGCTCTCCACCCGTAGACGCTGCGCGAAGTGAAGAGTGTGCGGGAACCAAGAGCTG 246

DB 223 AGCTCTCCACCCGTAGACGCTGCGCGAAGTGAAGAGTGTGCGGGAACCAAGAGCTG 288

QY 247 CTATGTTCTATGATGTGCTGAGAGAAACAGACCTGTCAACAGTTCAAGGGACGCTG 306

DB 289 CTATGTTCTATGATGTGCTGAGAGAAACAGACCTGTCAACAGTTCAAGGGACGCTG 348

QY 307 CGAGCGTTTCTCCAGCTCCCAAGTCCCGCTGGGTGAGTCCGAAATACCTGATTAACCTT 366
 DB 349 CGAGCGTTTCTCCAGCTCCCAAGTCCCGCTGGGTGAGTCCGAAATACCTGATTAACCTT 408
 QY 367 TTGAATGAGAGCGGCGCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
 DB 409 TTGAATGAGAGCGGCGCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
 QY 427 GCGAATGCCAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
 DB 469 GCGAATGCCAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
 QY 487 GCATTTGAGAGAGGAGGCGGCGGAGAAACAGACCTGATTTTCAGTCACTGCCAATGAGGCTG 546
 DB 529 GCATTTGAGAGAGGAGGCGGCGGAGAAACAGACCTGATTTTCAGTCACTGCCAATGAGGCTG 588
 QY 547 CCACTCCAGATCACTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
 DB 589 CCACTCCAGATCACTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
 QY 607 ATCTACAGCTTCAGTGTCCGAGAAATACAGCAAGTTCTTAAGCCACCTGCTTCTGCTG 666
 DB 649 ATCTACAGCTTCAGTGTCCGAGAAATACAGCAAGTTCTTAAGCCACCTGCTTCTGCTG 708
 QY 667 GAGTCCCGAGACTTTTCTGAGCA 690
 DB 709 GAGTCCCGAGACTTTTCTGAGCA 732

RESULT 12
 AX478528 1922 bp DNA linear PAT 12-AUG-2002
 LOCUS AX478528
 DEFINITION Sequence 32 from Patent WO0244209.
 ACCESSION AX478528
 VERSION AX478528.1 GI:22217300

KEYWORDS

SYNTHETIC CONSTRUCT

SYNTHETIC CONSTRUCT

ARTIFICIAL SEQUENCES

ORGANISM

1

PRESNELL, S.R., XU, W., NOVAK, J.E., WHITMORE, T.E. and GRANT, F.J.

CYTOKINE RECEPTOR ZCYTOR19

PATENT: WO 0244209-A 32 06-JUN-2002;

ZymoGenetics, Inc. (US)

LOCATION/Qualifiers

1. 1922

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/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="MBP-human zcytor19 fusion protein polynucleotide sequence"

123. 1922

/note="unnamed protein product"

/codon_start=1

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ANATVQLPBCMPPLDLKTVAPWKEGAKNTLPPTPGSQVQITLQPASEHSCSARTIT

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BASE COUNT 503 a 517 c 503 g 399 t

ORIGIN

Query Match 41.5%; Score 611.6; DB 6; Length 1922;

Best Local Similarity 97.0%; Pred. No. 2.2e-145;

QY 503 AGCCCCCTCTGGGCCCCCTCCCGAATGTGACGCTGCTCTCCCGAATCTCAAGCTGTAC 126

DB 109 AGCCCCCTCTGGGCCCCCTCCCGAATGTGACGCTGCTCTCCCGAATCTCAAGCTGTAC 168

QY 127 CTGACATGGCTCCGAGGCTTGGCAACCCCGAGATGTGACCTATTTTGGGCTATCAG 186

DB 169 CTGACATGGCTCCGAGGCTTGGCAACCCCGAGATGTGACCTATTTTGGGCTATCAG 228

QY 187 AGCTCTCCACCCGTAGACGCTGCGCGAAGTGAAGAGTGTGCGGGAACCAAGAGCTG 246

DB 223 AGCTCTCCACCCGTAGACGCTGCGCGAAGTGAAGAGTGTGCGGGAACCAAGAGCTG 288

QY 247 CTATGTTCTATGATGTGCTGAGAGAAACAGACCTGTCAACAGTTCAAGGGACGCTG 306

DB 289 CTATGTTCTATGATGTGCTGAGAGAAACAGACCTGTCAACAGTTCAAGGGACGCTG 348

ACCESSION	AY129153
VERSION	AY129153.1
KEYWORDS	GI-25527135
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE	Shepard, P.O., Presnell, S.R., Fox, B.A., Gilbert, T., Haldeman, B.A.
JOURNAL	IL28RA splice variant 3
RECORDS	Unpublished
FEATURES	2 (bases 1 to 674)
source	Shepard, P.O., Presnell, S.R., Fox, B.A., Gilbert, T., Haldeman, B.A. and Grant, P.J. Direct Submission Submitted (05-JUL-2002) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA Location/Qualifiers 1..674 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1..674 /gene="IL28RA" /note="synonym: zcytor19" 1..636 /gene="IL28RA" /note="alternatively spliced" /codon_start=1 /product="interleukin 28 receptor A splice variant 3" /protein_id="AAI28268.1" /db_xref="GI:25527136" /translation="MAGPERPGLICLLQAPRPRPLAPPVNTLSNPSVLTTLPGCLNDPVYFPAVYQSPTRRKREVREAGTKALCSMCVKRDLINKRKVFVSBSNSPWVESRIDTLPFEVRPPPLVLVTBISLISANATYPQPCMPDLDIKVEVAPEMGAGKNSSSPAPARQLPLHPPLRLRPSPQPAPAPLVLLQVFPVHS"
BASIS COUNT	128 a 223 c 182 g 141 t
ORIGIN	
Query Match	34.6%; Score 510; DB 9; Length 674;
Best Local Similarity	100.0%; Pred. No. 2.3e-119;
Matches 510; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Dd	1 ATGGCGGGGCCCGAAGCCTGGGGCCCCCTGTCTGTGGCTGTCGAAGCCGCTCAAGG 60
Oy	67 AGGCGCGGTGTGGCCCTTCCCGAATGTAGAAGCTCTCTCCGAACTTCAGCGTTAC 126
Dd	61 AGGCGCGGTGTGGCCCTTCCCGAATGTAGAAGCTCTCTCCGAACTTCAGCGTTAC 120
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Dd	181 AGCTCTCCCAACCGGTAGAGGTGGGGGGAAGTGAAGATGTGGCGAACCAAGAGACTG 240
Oy	247 CTAATTTCTATGATGTGCTTGAAAGAAAGAGACTTGTACAACAATTCAGAGACCGCTG 306
Dd	241 CTAATTTCTATGATGTGCTTGAAAGAAAGAGACTTGTACAACAATTCAGAGACCGCTG 300
Oy	307 CGGACGGTTTTCTCCCAAGCTCCAGTGCCCGCTGGGTGAGTCCGAAATACCTGATTACCT 366
Dd	301 CGGACGGTTTTCTCCCAAGCTCCAGTGCCCGCTGGGTGAGTCCGAAATACCTGATTACCT 360
Oy	367 TTATGAAGTAGAGGCGGCGCCCACTGTCTCTGTGGCTACACCAAGAGAGATCTTGAGT 426
Dd	361 TTATGAAGTAGAGGCGGCGCCCACTGTCTCTGTGGCTACACCAAGAGAGATCTTGAGT 420
Oy	427 GCCAATGCACGTATCACAGCTGCCCCCTGTGATGCCCACTGAGTCTGAAGTATGAGTG 486

Db 421 GGCATATGCAATGTTCCAGCTGCCCCCTCGATGCCCCCACTGATCTGAATGATGAGTGG 480

Qy 487 GCATTCTGGAAGAGGAGGCGGAAACAG 516

Db 481 GCATTCTGGAAGAGGAGGCGGAAACAG 510

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